FIGURE 3A

FIGURE 3B

```
                441                                                                                    550
original  BCY1   (438)  GTTCGAGAATCACGGGCTGCCTCCAGGCAACGGTGAGAGGAGAGGAGGACGACGACGCACATGCGGTGCGCACTGGAGTACAACGAAGCATGAAAAACGACT
MC50A19 BCY I    (411)  GTTCGAGAATCACGGGCTGCCTCCAGGCAACGGTGAGAGGAGAGGAGGACGACGACGCACATGCGGTGCGCACTGGAGTACAACGAAGCATGAAAAACGACT
MC50A6  BCY I    (411)  GTTCGAGAATCACGGGCTGCCTCCAGGCAACGGTGAGAGGAGAGGAGGACGACGACGCACATGCGGTGCGCACTGGAGTACAACGAAGCATGAAAAACGACT
MC50A8  BCY I    (411)  GTTCGAGAATCACGGGCTGCCTCCAGGCAACGGTGAGAGGAGAGGAGGACGACGACGCACATGCGGTGCGCACTGGAGTACAACGAAGCATGAAAAACGACT
MC54.21 BCY I    (411)  GTTCGAGAATCACGGGCTGCCTCCAGGCAACGGTGAGAGGAGAGGAGGACGACGACGCACATGCGGTGCGCACTGGAGTACAACGAAGCATGAAAAACGACT
MC55.29 BCY I    (411)  GTTCGAGAATCACGGGCTGCCTCCAGGCAACGGTGAGAGGAGAGGAGGACGACGACGCACATGCGGTGCGCACTGGAGTACAACGAAGCATGAAAAACGACT
MC55.32 BCY I    (411)  GTTCGAGAATCACGGGCTGCCTCCAGGCAACGGTGAGAGGAGAGGAGGACGACGACGCACATGCGGTGCGCACTGGAGTACAACGAAGCATGAAAAACGACT
     Consensus   (441)  GTTCGAGAATCACGGGCTGCCTCCAGGCAACGGTGAGAGGAGAGGAGGACGACGACGCACATGCGGTGCGCACTGGAGTACAACGAAGCATGAAAAACGACT

                551                                                                                    660
original  BCY1   (548)  TCCTGGCGGGGGAGCCCGACGACGCAGCAAATCGAATAGCCTACTCCGACGCCTCGCCGGGTGCACAGGCCCTCTCCTACCTTTCCGGGCCAGAACAGCCTTGGGC
MC50A19 BCY I    (551)  TCCTGGCGGGGGAGCCCGACGACGCAGCAAATCGAATAGCCTACTCCGACGCCTCGCCGGGTGCACAGGCCCTCTCCTACCTTTCCGGGCCAGAACAGCCTTGGGC
MC50A6  BCY I    (551)  TCCTGGCGGGGGAGCCCGACGACGCAGCAAATCGAATAGCCTACTCCGACGCCTCGCCGGGTGCACAGGCCCTCTCCTACCTTTCCGGGCCAGAACAGCCTTGGGC
MC50A8  BCY I    (551)  TCCTGGCGGGGGAGCCCGACGACGCAGCAAATCGAATAGCCTACTCCGACGCCTCGCCGGGTGCACAGGCCCTCTCCTACCTTTCCGGGCCAGAACAGCCTTGGGC
MC54.21 BCY I    (551)  TCCTGGCGGGGGAGCCCGACGACGCAGCAAATCGAATAGCCTACTCCGACGCCTCGCCGGGTGCACAGGCCCTCTCCTACCTTTCCGGGCCAGAACAGCCTTGGGC
MC55.29 BCY I    (551)  TCCTGGCGGGGGAGCCCGACGACGCAGCAAATCGAATAGCCTACTCCGACGCCTCGCCGGGTGCACAGGCCCTCTCCTACCTTTCCGGGCCAGAACAGCCTTGGGC
MC55.32 BCY I    (551)  TCCTGGCGGGGGAGCCCGACGACGCAGCAAATCGAATAGCCTACTCCGACGCCTCGCCGGGTGCACAGGCCCTCTCCTACCTTTCCGGGCCAGAACAGCCTTGGGC
     Consensus   (551)  TCCTGGCGGGGGAGCCCGACGACGCAGCAAATCGAATAGCCTACTCCGACGCCTCGCCGGGTGCACAGGCCCTCTCCTACCTTTCCGGGCCAGAACAGCCTTGGGC

                661                                                                                    770
original  BCY1   (658)  TGCATCCGGCGGAGTGCGGAGTGGAACTGTCTGGCTTTTGCAGCGCCCACACCTGGGTGAGCAGGACGGGGGAAATTTGGCACAGCGGTGGGTACCCTTCTTCCTGGGTTATGGCGTGGGCAA
MC50A19 BCY I    (661)  TGCATCCGGCGGAGTGCGGAGTGGAACTGTCTGGCTTTTGCAGCGCCCACACCTGGGTGAGCAGGACGGGGGAAATTTGGCACAGCGGTGGGTACCCTTCTTCCTGGGTTATGGCGTGGGCAA
MC50A6  BCY I    (661)  TGCATCCGGCGGAGTGCGGAGTGGAACTGTCTGGCTTTTGCAGCGCCCACACCTGGGTGAGCAGGACGGGGGAAATTTGGCACAGCGGTGGGTACCCTTCTTCCTGGGTTATGGCGTGGGCAA
MC50A8  BCY I    (661)  TGCATCCGGCGGAGTGCGGAGTGGAACTGTCTGGCTTTTGCAGCGCCCACACCTGGGTGAGCAGGACGGGGGAAATTTGGCACAGCGGTGGGTACCCTTCTTCCTGGGTTATGGCGTGGGCAA
MC54.21 BCY I    (661)  TGCATCCGGCGGAGTGCGGAGTGGAACTGTCTGGCTTTTGCAGCGCCCACACCTGGGTGAGCAGGACGGGGGAAATTTGGCACAGCGGTGGGTACCCTTCTTCCTGGGTTATGGCGTGGGCAA
MC55.29 BCY I    (661)  TGCATCCGGCGGAGTGCGGAGTGGAACTGTCTGGCTTTTGCAGCGCCCACACCTGGGTGAGCAGGACGGGGGAAATTTGGCACAGCGGTGGGTACCCTTCTTCCTGGGTTATGGCGTGGGCAA
MC55.32 BCY I    (661)  TGCATCCGGCGGAGTGCGGAGTGGAACTGTCTGGCTTTTGCAGCGCCCACACCTGGGTGAGCAGGACGGGGGAAATTTGGCACAGCGGTGGGTACCCTTCTTCCTGGGTTATGGCGTGGGCAA
     Consensus   (661)  TGCATCCGGCGGAGTGCGGAGTGGAACTGTCTGGCTTTTGCAGCGCCCACACCTGGGTGAGCAGGACGGGGGAAATTTGGCACAGCGGTGGGTACCCTTCTTCCTGGGTTATGGCGTGGGCAA

                771                                                                                    880
original  BCY1   (768)  GCAGGATGTGTGTACTACGGCGTGGCCGGCGAGAACCACCAGAGAAGAACGACAGAGAGAACGCCACCGCCACCCGTGCTCTTCTCTCTTCTCTCCTCTCTT
MC50A19 BCY I    (771)  GCAGGATGTGTGTACTACGGCGTGGCCGGCGAGAACCACCAGAGAAGAACGACAGAGAGAACGCCACCGCCACCCGTGCTCTTCTCTCTTCTCTCCTCTCTT
MC50A6  BCY I    (771)  GCAGGATGTGTGTACTACGGCGTGGCCGGCGAGAACCACCAGAGAAGAACGACAGAGAGAACGCCACCGCCACCCGTGCTCTTCTCTCTTCTCTCCTCTCTT
MC50A8  BCY I    (771)  GCAGGATGTGTGTACTACGGCGTGGCCGGCGAGAACCACCAGAGAAGAACGACAGAGAGAACGCCACCGCCACCCGTGCTCTTCTCTCTTCTCTCCTCTCTT
MC54.21 BCY I    (771)  GCAGGATGTGTGTACTACGGCGTGGCCGGCGAGAACCACCAGAGAAGAACGACAGAGAGAACGCCACCGCCACCCGTGCTCTTCTCTCTTCTCTCCTCTCTT
MC55.29 BCY I    (771)  GCAGGATGTGTGTACTACGGCGTGGCCGGCGAGAACCACCAGAGAAGAACGACAGAGAGAACGCCACCGCCACCCGTGCTCTTCTCTCTTCTCTCCTCTCTT
MC55.32 BCY I    (771)  GCAGGATGTGTGTACTACGGCGTGGCCGGCGAGAACCACCAGAGAAGAACGACAGAGAGAACGCCACCGCCACCCGTGCTCTTCTCTCTTCTCTCCTCTCTT
     Consensus   (771)  GCAGGATGTGTGTACTACGGCGTGGCCGGCGAGAACCACCAGAGAAGAACGACAGAGAGAACGCCACCGCCACCCGTGCTCTTCTCTCTTCTCTCCTCTCTT
```

FIGURE 3C

```
                       881                                                                                                 990
original BCY1  (878)  CTTCCGCCAAGGCCGGCGCTGGGGCCCCGGGGCGACACGGCCCCCTGCCCACTTCCGGAGGCCGGACCCGGAGCTGGCGGAGCCCCGGAGGGAGGCGGCTCCAG
MC50A19 BCY I  (861)  CTTCCGCCAAGGCCGGCGCTGGGGCCCCGGGGCGACACGGCCCCCTGCCCACTTCCGGAGGCCGGACCCGGAGCTGGCGGAGCCCCGGAGGGAGGCGGCTCCAG
MC50A6 BCY I   (861)  CTTCCGCCAAGGCCGGCGCTGGGGCCCCGGGGCGACACGGCCCCCTGCCCACTTCCGGAGGCCGGACCCGGAGCTGGCGGAGCCCCGGAGGGAGGCGGCTCCAG
MC50A8 BCY I   (861)  CTTCCGCCAAGGCCGGCGCTGGGGCCCCGGGGCGACACGGCCCCCTGCCCACTTCCGGAGGCCGGACCCGGAGCTGGCGGAGCCCCGGAGGGAGGCGGCTCCAG
MC54.21 BCY I  (861)  CTTCCGCCAAGGCCGGCGCTGGGGCCCCGGGGCGACACGGCCCCCTGCCCACTTCCGGAGGCCGGACCCGGAGCTGGCGGAGCCCCGGAGGGAGGCGGCTCCAG
MC55.29 BCY I  (861)  CTTCCGCCAAGGCCGGCGCTGGGGCCCCGGGGCGACACGGCCCCCTGCCCACTTCCGGAGGCCGGACCCGGAGCTGGCGGAGCCCCGGAGGGAGGCGGCTCCAG
MC55.32 BCY I  (861)  CTTCCGCCAAGGCCGGCGCTGGGGCCCCGGGGCGACACGGCCCCCTGCCCACTTCCGGAGGCCGGACCCGGAGCTGGCGGAGCCCCGGAGGGAGGCGGCTCCAG
Consensus             CTTCCGCCAAGGCCGGCGCTGGGGCCCCGGGGCGACACGGCCCCCTGCCCACTTCCGGAGGCCGGACCCGGAGCTGGCGGAGCCCCGGAGGGAGGCGGCTCCAG

                       991                                                                                                 1100
original BCY1  (968)  GGCTTCTCTAAACTTGGTGGGGGCGGCCTCGCGGAGCCCGGGCAGCCGGGCGGAGGCGGGGAGGATTGCATGGGCCTGCTTTGAGGACGCAAGGTGATCGCCGC
MC50A19 BCY I  (991)  GGCTTCTCTAAACTTGGTGGGGGCGGCCTCGCGGAGCCCGGG---CGGCGGCGGGCGGAGGCGGGGAGGATTGCATGGGCCTGCTTTGAGGACGCAAGGTGATCGCCGC
MC50A6 BCY I   (991)  GGCTTCTCTAAACTTGGTGGGGGCGGCCTCGCGGAGCCCGGG---CGGCGGCGGGCGGAGGCGGGGAGGATTGCATGGGCCTGCTTTGAGGACGCAAGGTGATCGCCGC
MC50A8 BCY I   (991)  GGCTTCTCTAAACTTGGTGGGGGCGGCCTCGCGGAGCCCGGG---CGGCGGCGGGCGGAGGCGGGGAGGATTGCATGGGCCTGCTTTGAGGACGCAAGGTGATCGCCGC
MC54.21 BCY I  (991)  GGCTTCTCTAAACTTGGTGGGGGCGGCCTCGCGGAGCCCGGG---CGGCGGCGGGCGGAGGCGGGGAGGATTGCATGGGCCTGCTTTGAGGACGCAAGGTGATCGCCGC
MC55.29 BCY I  (991)  GGCTTCTCTAAACTTGGTGGGGGCGGCCTCGCGGAGCCCGGG---CGGCGGCGGGCGGAGGCGGGGAGGATTGCATGGGCCTGCTTTGAGGACGCAAGGTGATCGCCGC
MC55.32 BCY I  (991)  GGCTTCTCTAAACTTGGTGGGGGCGGCCTCGCGGAGCCCGGG---CGGCGGCGGGCGGAGGCGGGGAGGATTGCATGGGCCTGCTTTGAGGACGCAAGGTGATCGCCGC
Consensus             GGCTTCTCTAAACTTGGTGGGGGCGGCCTCGCGGAGCCCGGG   CGGCGGCGGGCGGAGGCGGGGAGGATTGCATGGGCCTGCTTTGAGGACGCAAGGTGATCGCCGC

                       1101                                                                                                1210
original BCY1  (1098) CAACTGTTCTCGCATGGAGTCAGTACGTCAGTACGCATCTGCGACAGGACGGACCCCAGATGTCCGTGTGCACATCACAGTCACCACAGATATTCTCCTAA
MC50A19 BCY I  (1098) CAACTGTTCTCGCATGGAGTCAGTACGTCAGTACGCATCTGCGACAGGACGGACCCCAGATGTCCGTGTGCACATCACAGTCACCACAGATATTCTCCAAGGAT
MC50A6 BCY I   (1098) CAACTGTTCTCGCATGGAGTCAGTACGTCAGTACGCATCTGCGACAGGACGGACCCCAGATGTCCGTGTGCACATCACAGTCACCACAGATATTCTCCAAGGAT
MC50A8 BCY I   (1098) CAACTGTTCTCGCATGGAGTCAGTACGTCAGTACGCATCTGCGACAGGACGGACCCCAGATGTCCGTGTGCACATCACAGTCACCACAGATATTCTCCAAGGAT
MC54.21 BCY I  (1098) CAACTGTTCTCGCATGGAGTCAGTACGTCAGTACGCATCTGCGACAGGACGGACCCCAGATGTCCGTGTGCACATCACAGTCACCACAGATATTCTCCTAA----
MC55.29 BCY I  (1098) CAACTGTTCTCGCATGGAGTCAGTACGTCAGTACGCATCTGCGACAGGACGGACCCCAGATGTCCGTGTGCACATCACAGTCACCACAGATATTCTCCTAA----
MC55.32 BCY I  (1101) CAACTGTTCTCGCATGGAGTCAGTACGTCAGTACGCATCTGCGACAGGACGGACCCCAGATGTCCGTGTGCACATCACAGTCACCACAGATATTCTCCTAA----
Consensus             CAACTGTTCTCGCATGGAGTCAGTACGTCAGTACGCATCTGCGACAGGACGGACCCCAGATGTCCGTGTGCACATCACAGTCACCACAGATATTCTCCTAA

                       1211                                      1249
original BCY1  (1204) CCACTAGTCCCAGTGTGGTTGGTGGAATTCTCGAGATATCCA
MC50A19 BCY I  (1208) CCACTAGTCCCAGTGTGGTTGGTGGAATTCTCGAGATATCCA-
MC50A6 BCY I   (1208) CCACTAGTCCCAGTGTGGTTGGTGGAATTCTCGAGATATCCA-
MC50A8 BCY I   (1208) CCACTAGTCCCAGTGTGGTTGGTGGAATTCTCGAGATATCCAG
MC54.21 BCY I  (1204) -----------------------------------------
MC55.29 BCY I  (1204) -----------------------------------------
MC55.32 BCY I  (1204) -----------------------------------------
Consensus
```

FIGURE 3D

```
MAELRLKGSS NTTECPVPVT SEHVAEIVGR QGCKIKALRA KTNTYIKTPV RGEEPVFMVT GREEDVATAR REIISAAEHF SMIRASRNKS
GAAFGVAPAL PGQVTIRVRV PYRVVGLVVG PKGATIKRIQ QQTNTYIITP SRDRDPVFEI TGAPGNVERA REEIETHIAV RTGKILEYNN
ENEFLAGSPD AAIDSRYSPA WRVHQPGCKP LSTFPQNSLG CIGEGGVDSG FEAPRLGEQG GDFGYGGYLF PGYGVGKQPV YYGVAETSPP
LMAGQENAIP TSVLFSSASS SSSSSAKARA GPFGAHRSPA TSAGPELAGL PRRPPGEPLQ GFSKLGGGGL RSPGGGRDCM VCFESEVTAA
LVFCGHNLFC MECAVRLICER TDPECPVCHI TAAGAIRIFS
```